

10049710**PCT10****RAW SEQUENCE LISTING**

DATE: 01/04/2003

PATENT APPLICATION: **US/10/049,710A**

TIME: 20:49:11

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1 <110> APPLICANT: Shinmyo, Atsuhiko
2 Kato, Kou
3 Yamada, Yasuhiro
4 Nihira, Takuya
5 Shindo, Takuya
6 <120> TITLE OF INVENTION: METHOD FOR INDUCTION OF GENE EXPRESSION IN PLANT AND PLANT
TREATED
7 THEREBY
8 <130> FILE REFERENCE: 5405/18
C--> 9 <140> **CURRENT APPLICATION NUMBER: US/10/049,710A**
10 <141> CURRENT FILING DATE: 2002-02-15
11 <150> PRIOR APPLICATION NUMBER: PCT/JP01/05096
12 <151> PRIOR FILING DATE: 2001-06-15
13 <150> PRIOR APPLICATION NUMBER: JP 2000-180466
14 <151> PRIOR FILING DATE: 2000-06-15
15 <160> NUMBER OF SEQ ID NOS: 11
16 <170> SOFTWARE: PatentIn version 3.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 699
20 <212> TYPE: DNA
21 <213> ORGANISM: Streptomyces virginiae
22 <220> FEATURE:
23 <221> NAME/KEY: CDS
24 <222> LOCATION: (1)..(699)
25 <223> OTHER INFORMATION:
26 <300> PUBLICATION INFORMATION:
27 <301> AUTHORS: Okamoto, S., Nakamura, K., Nihira, T. and Yamada, Y.
28 <302> TITLE: Virginiae butanolide binding protein from Streptomyces virginiae.
29 Evidence that VbrA is not the virginiae butanolide binding protein and re-
30 identification of the true binding protein
31 <303> JOURNAL: Journal of Biological Chemistry
32 <304> VOLUME: 270
33 <305> ISSUE: 20
34 <306> PAGES: 12319-12326
35 <307> DATE: 1995-05-19
36 <308> DATABASE ACCESSION NO: D32251
37 <309> DATABASE ENTRY DATE: 1994-07-19
38 <313> RELEVANT RESIDUES: (1)..(699)
39 <300> PUBLICATION INFORMATION:
40 <301> AUTHORS: Okamoto, S., Nakamura, K., Nihira, T. and Yamada, Y.
41 <302> TITLE: Virginiae butanolide binding protein from Streptomyces virginiae.
42 Evidence that VbrA is not the virginiae butanolide binding protein and re-
43 identification of the true binding protein

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44 <303> JOURNAL: Journal of Biological Chemistry

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 46 <305> ISSUE: 20
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 48 <307> DATE: 1995-05-19
 49 <308> DATABASE ACCESSION NO: D32251
 50 <309> DATABASE ENTRY DATE: 1994-07-19

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55	cgc acg cgg cag gcg atc gtg cgg gca gcc gcc tcg gtc ttc gac gag	96
56	Arg Thr Arg Gln Ala Ile Val Arg Ala Ala Ala Ser Val Phe Asp Glu	
57	20 25 30	
58	tac ggg ttc gag gcc gcc aca gtg gca gag atc ctc tcg cgg gcc tcg	144
59	Tyr Gly Phe Glu Ala Ala Thr Val Ala Glu Ile Leu Ser Arg Ala Ser	
60	35 40 45	
61	gtc acc aag ggc gcg atg tac ttc cac ttc gct tcc aag gaa gag ctg	192
62	Val Thr Lys Gly Ala Met Tyr Phe His Phe Ala Ser Lys Glu Glu Leu	
63	50 55 60	
64	gcc cgc ggc gtg ctg gcc gag cag acc ctg cac gtg gcg gtg ccg gaa	240
65	Ala Arg Gly Val Leu Ala Glu Gln Thr Leu His Val Ala Val Pro Glu	
66	65 70 75 80	
67	tcc ggc tcc aag gcg cag gaa ctg gta gac ctc acc atg ctg gtc gcc	288
68	Ser Gly Ser Lys Ala Gln Glu Leu Val Asp Leu Thr Met Leu Val Ala	
69	85 90 95	
70	cac ggc atg ctg cac gat ccg atc ctg cgg gcg ggc acg cgg ctc gca	336
71	His Gly Met Leu His Asp Pro Ile Leu Arg Ala Gly Thr Arg Leu Ala	
72	100 105 110	
73	ctg gac cag ggg gcg gtg gac ttc tcc gac gcc aac ccg ttc ggc gag	384
74	Leu Asp Gln Gly Ala Val Asp Phe Ser Asp Ala Asn Pro Phe Gly Glu	
75	115 120 125	
76	tgg ggc gac atc tgc gcc cag ctc ctg gcg gag gca cag gaa cgg ggg	432
77	Trp Gly Asp Ile Cys Ala Gln Leu Leu Ala Glu Ala Gln Glu Arg Gly	
78	130 135 140	
79	gag gtg ctt ccg cac gtg aac ccg aaa aag acc ggc gac ttc atc gtc	480
80	Glu Val Leu Pro His Val Asn Pro Lys Lys Thr Gly Asp Phe Ile Val	
81	145 150 155 160	
82	ggc tgc ttc acc ggg ctc cag gcg gtc tcc ccg gtc acc tcc gac cgc	528
83	Gly Cys Phe Thr Gly Leu Gln Ala Val Ser Arg Val Thr Ser Asp Arg	
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85	cag gac ctc ggc cac cgg atc tcg gtg atg tgg aac cac gtg ctg ccc	576
86	Gln Asp Leu Gly His Arg Ile Ser Val Met Trp Asn His Val Leu Pro	
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88	agc atc gtg ccg gcg tcc atg ctg acc tgg atc gaa acc ggc gag gag	624
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92	Arg Ile Gly Lys Val Ala Ala Ala Glu Ala Ala Glu Ala Ala Glu	
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 108 35 40 45
 109 Val Thr Lys Gly Ala Met Tyr Phe His Phe Ala Ser Lys Glu Glu Leu
 110 50 55 60
 111 Ala Arg Gly Val Leu Ala Glu Gln Thr Leu His Val Ala Val Pro Glu
 112 65 70 75 80
 113 Ser Gly Ser Lys Ala Gln Glu Leu Val Asp Leu Thr Met Leu Val Ala
 114 85 90 95
 115 His Gly Met Leu His Asp Pro Ile Leu Arg Ala Gly Thr Arg Leu Ala
 116 100 105 110
 117 Leu Asp Gln Gly Ala Val Asp Phe Ser Asp Ala Asn Pro Phe Gly Glu
 118 115 120 125
 119 Trp Gly Asp Ile Cys Ala Gln Leu Leu Ala Glu Ala Gln Glu Arg Gly
 120 130 135 140
 121 Glu Val Leu Pro His Val Asn Pro Lys Lys Thr Gly Asp Phe Ile Val
 122 145 150 155 160
 123 Gly Cys Phe Thr Gly Leu Gln Ala Val Ser Arg Val Thr Ser Asp Arg
 124 165 170 175
 125 Gln Asp Leu Gly His Arg Ile Ser Val Met Trp Asn His Val Leu Pro
 126 180 185 190
 127 Ser Ile Val Pro Ala Ser Met Leu Thr Trp Ile Glu Thr Gly Glu Glu
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 137 <213> ORGANISM: Streptomyces virginiae
 138 <300> PUBLICATION INFORMATION:
 139 <301> AUTHORS: Kinoshita, H., Tsuji, T., Ipposhi, H., Nihira, T. and Yamada, Y.
 140 <302> TITLE: Characterization of Binding Sequences for Butyrolactone Autoregulator
 141 Receptors in Streptomycetes
 142 <303> JOURNAL: Journal of Bacteriology
 143 <304> VOLUME: 181
 144 <305> ISSUE: 16

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149 <313> RELEVANT RESIDUES: (1)..(26)
150 <300> PUBLICATION INFORMATION:
151 <301> AUTHORS: Kinoshita, H., Tsuji, T., Ipposhi, H., Nihira, T. and Yamada, Y.
152 <302> TITLE: Characterization of Binding Sequences for Butyrolactone Autoregulator
153       Receptors in Streptomyces
154 <303> JOURNAL: Journal of Bacteriology
155 <304> VOLUME: 181
156 <305> ISSUE: 16
157 <306> PAGES: 5075-5080
158 <307> DATE: 1999-08
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169 <223> OTHER INFORMATION: Designed sequence of the CamV 35S promoter modified to
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170       operator BARE-3 element just downstream of its TAT-box
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183       gatattctcca ctgacgtaag g gatgacgca caatcagata cataccaacc ggttcttttg      60
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204 <400> SEQUENCE: 7
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215     enzyme BamH I recognition sequence for PCR amplification of the barA gene
216     coding region to be cloned by cut with the enzyme
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226     enzyme Sac I recognition sequence for PCR amplification of the barA gene
227     coding region to be cloned by cut with the enzyme
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238     just downstream and upstream of its TATA-box
239 <400> SEQUENCE: 10
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246 <213> ORGANISM: Artificial sequence
247 <220> FEATURE:
248 <223> OTHER INFORMATION: Designed sequence of the other of paired oligo DNAs for
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249     of the modified CaMV 35S promoter containing three of the operator BARE-3

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